

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,561
Source: PCT
Date Processed by STIC: 11/1/04

ENTERED

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 10/511,561

CRF Edit Date: 11/1/04
Edited by: TL

 Realigned nucleic acid/amino acid numbers/text in cases where the sequence
text "wrapped" to the next line

 Corrected the SEQ ID NO. Sequence numbers edited were:

 Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID
NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; page numbers

 Inserted mandatory headings/numeric identifiers, specifically:

 Moved responses to same line as heading/numeric identifier, specifically:

 Other:



PCT

RAW SEQUENCE LISTING

DATE: 11/01/2004

PATENT APPLICATION: US/10/511,561

TIME: 11:54:09

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10292004\J511561.raw

2 <110> APPLICANT: Chan, Doug W
 3 Chen, Ping-Chi B
 4 Chen, David J
 6 <120> TITLE OF INVENTION: DNA Dependent Protein Kinase Catalytic Subunit
 Phosphorylation Sites
 7 and Antibodies Thereto
 W--> 8 <130> FILE REFERENCE: IB-1807 PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/511,561
 C--> 12 <141> CURRENT FILING DATE: 2004-10-15
 14 <150> PRIOR APPLICATION NUMBER: US 60/375,094
 16 <151> PRIOR FILING DATE: 2002-04-22
 18 <160> NUMBER OF SEQ ID NOS: 28
 20 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 26 <211> LENGTH: 14
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <221> NAME/KEY: PEPTIDE
 32 <222> LOCATION: (1)..(14)
 33 <223> OTHER INFORMATION: HUMAN GENETIC ORIGIN
 35 <220> FEATURE:
 36 <221> NAME/KEY: MOD_RES
 37 <222> LOCATION: (7)..(7)
 38 <223> OTHER INFORMATION: PHOSPHORYLATION at T2609
 40 <400> SEQUENCE: 1
 42 Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Cys
 43 1 5 10
 46 <210> SEQ ID NO: 2
 48 <211> LENGTH: 14
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Artificial Sequence
 52 <220> FEATURE:
 53 <221> NAME/KEY: PEPTIDE
 54 <222> LOCATION: (1)..(14)
 55 <223> OTHER INFORMATION: HUMAN GENETIC ORIGIN
 57 <220> FEATURE:
 58 <221> NAME/KEY: MOD_RES
 59 <222> LOCATION: (7)..(7)
 60 <223> OTHER INFORMATION: PHOSPHORYLATION at S2056
 62 <400> SEQUENCE: 2
 64 Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro Arg Pro Ala Cys
 65 1 5 10
 68 <210> SEQ ID NO: 3

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Input Set : A:\pto.kd.txt

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70 <211> LENGTH: 4128

71 <212> TYPE: PRT

72 <213> ORGANISM: Homo sapiens

74 <400> SEQUENCE: 3

76 Met Ala Gly Ser Gly Ala Gly Val Arg Cys Ser Leu Leu Arg Leu Gln

77 1 5 10 15

80 Glu Thr Leu Ser Ala Ala Asp Arg Cys Gly Ala Ala Leu Ala Gly His

81 20 25 30

84 Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro

85 35 40 45

88 Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly

89 50 55 60

92 Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu

93 65 70 75 80

96 Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met

97 85 90 95

100 Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr

101 100 105 110

104 Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu

105 115 120 125

108 Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met

109 130 135 140

112 Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu

113 145 150 155 160

116 Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu

117 165 170 175

120 Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn

121 180 185 190

124 Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met

125 195 200 205

128 Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu

129 210 215 220

132 Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu

133 225 230 235 240

136 Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile

137 245 250 255

140 Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu

141 260 265 270

144 Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp

145 275 280 285

148 Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr

149 290 295 300

152 Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu

153 305 310 315 320

156 Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn

157 325 330 335

160 Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val

161 340 345 350

164 Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu

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Input Set : A:\pto.kd.txt

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165          355          360          365
168 Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met
169          370          375          380
172 Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
173 385          390          395          400
176 Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
177          405          410          415
180 Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
181          420          425          430
184 Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
185          435          440          445
188 Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
189          450          455          460
192 Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
193 465          470          475          480
196 Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
197          485          490          495
200 Leu Pro Lys Gly Pro Glu Ser Glu Ser Glu Asp His Arg Ala Ser Gly
201          500          505          510
204 Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
205          515          520          525
208 Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile
209          530          535          540
212 Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu
213 545          550          555          560
216 Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
217          565          570          575
220 Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
221          580          585          590
224 Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
225          595          600          605
228 Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile
229          610          615          620
232 Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu
233 625          630          635          640
236 Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln
237          645          650          655
240 Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile
241          660          665          670
244 Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro
245          675          680          685
248 Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe
249          690          695          700
252 Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln
253 705          710          715          720
256 Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu
257          725          730          735
260 Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu
261          740          745          750

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264 Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val
265           755           760           765
268 Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val
269       770           775           780
272 Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu
273 785           790           795           800
276 Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser
277           805           810           815
280 Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys
281           820           825           830
284 His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu
285           835           840           845
288 Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
289       850           855           860
292 Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
293 865           870           875           880
296 Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
297           885           890           895
300 Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
301           900           905           910
304 Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val
305       915           920           925
308 Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
309       930           935           940
312 Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
313 945           950           955           960
316 Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val
317           965           970           975
320 Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
321       980           985           990
324 His Trp Phe Thr Asn Asn Lys Lys Phe Glu Ser Gln Asp Thr Val Ser
325       995           1000           1005
328 Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser
329       1010           1015           1020
332 Thr Leu Arg Asp Phe Cys Gly Arg Cys Ile Arg Glu Phe Leu Lys
333       1025           1030           1035
336 Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Gln Glu Lys Ser Pro
337       1040           1045           1050
340 Val Asn Thr Lys Ser Leu Phe Lys Arg Leu Tyr Ser Leu Ala Leu
341       1055           1060           1065
344 His Pro Asn Ala Phe Lys Arg Leu Gly Ala Ser Leu Ala Phe Asn
345       1070           1075           1080
348 Asn Ile Tyr Arg Glu Phe Arg Glu Glu Glu Ser Leu Val Glu Gln
349       1085           1090           1095
352 Phe Val Phe Glu Ala Leu Val Ile Tyr Met Glu Ser Leu Ala Leu
353       1100           1105           1110
356 Ala His Ala Asp Glu Lys Ser Leu Gly Thr Ile Gln Gln Cys Cys
357       1115           1120           1125
360 Asp Ala Ile Asp His Leu Cys Arg Ile Ile Glu Lys Lys His Val

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| | | | | | |
|-----|---|--|------|--|------|
| 361 | 1130 | | 1135 | | 1140 |
| 364 | Ser Leu Asn Lys Ala Lys Lys Arg Arg Leu Pro Arg Gly Phe Pro | | | | |
| 365 | 1145 | | 1150 | | 1155 |
| 368 | Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu | | | | |
| 369 | 1160 | | 1165 | | 1170 |
| 372 | Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile | | | | |
| 373 | 1175 | | 1180 | | 1185 |
| 376 | Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser | | | | |
| 377 | 1190 | | 1195 | | 1200 |
| 380 | Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser | | | | |
| 381 | 1205 | | 1210 | | 1215 |
| 384 | Phe Leu Ile Asn Thr Phe Glu Gly Gly Gly Cys Gly Gln Pro Ser | | | | |
| 385 | 1220 | | 1225 | | 1230 |
| 388 | Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe | | | | |
| 389 | 1235 | | 1240 | | 1245 |
| 392 | Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala | | | | |
| 393 | 1250 | | 1255 | | 1260 |
| 396 | Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala | | | | |
| 397 | 1265 | | 1270 | | 1275 |
| 400 | Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala | | | | |
| 401 | 1280 | | 1285 | | 1290 |
| 404 | Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala | | | | |
| 405 | 1295 | | 1300 | | 1305 |
| 408 | Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser | | | | |
| 409 | 1310 | | 1315 | | 1320 |
| 412 | Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val | | | | |
| 413 | 1325 | | 1330 | | 1335 |
| 416 | Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro | | | | |
| 417 | 1340 | | 1345 | | 1350 |
| 420 | Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu | | | | |
| 421 | 1355 | | 1360 | | 1365 |
| 424 | Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly | | | | |
| 425 | 1370 | | 1375 | | 1380 |
| 428 | Phe Asn Ile Gly Asp Val Gln Val Met Ala His Leu Pro Asp Val | | | | |
| 429 | 1385 | | 1390 | | 1395 |
| 432 | Cys Val Asn Leu Met Lys Ala Leu Lys Met Ser Pro Tyr Lys Asp | | | | |
| 433 | 1400 | | 1405 | | 1410 |
| 436 | Ile Leu Glu Thr His Leu Arg Glu Lys Ile Thr Ala Gln Ser Ile | | | | |
| 437 | 1415 | | 1420 | | 1425 |
| 440 | Glu Glu Leu Cys Ala Val Asn Leu Tyr Gly Pro Asp Ala Gln Val | | | | |
| 441 | 1430 | | 1435 | | 1440 |
| 444 | Asp Arg Ser Arg Leu Ala Ala Val Val Ser Ala Cys Lys Gln Leu | | | | |
| 445 | 1445 | | 1450 | | 1455 |
| 448 | His Arg Ala Gly Leu Leu His Asn Ile Leu Pro Ser Gln Ser Thr | | | | |
| 449 | 1460 | | 1465 | | 1470 |
| 452 | Asp Leu His His Ser Val Gly Thr Glu Leu Leu Ser Leu Val Tyr | | | | |
| 453 | 1475 | | 1480 | | 1485 |
| 456 | Lys Gly Ile Ala Pro Gly Asp Glu Arg Gln Cys Leu Pro Ser Leu | | | | |
| 457 | 1490 | | 1495 | | 1500 |

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,561

DATE: 11/01/2004

TIME: 11:54:10

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10292004\J511561.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date



PCT

RAW SEQUENCE LISTING

DATE: 10/26/2004

PATENT APPLICATION: US/10/511,561

TIME: 17:50:28

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10262004\J511561.raw

2 <110> APPLICANT: Chan, Doug W

3 Chen, Ping-Chi B

4 Chen, David J

6 <120> TITLE OF INVENTION: DNA Dependent Protein Kinase Catalytic Subunit

Phosphorylation Sites

7 and Antibodies Thereto

W--> 8 <130> FILE REFERENCE: IB-1807 PCT

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/511,561

C--> 12 <141> CURRENT FILING DATE: 2004-10-15

14 <150> PRIOR APPLICATION NUMBER: US 60/375,094

16 <151> PRIOR FILING DATE: 2002-04-22

18 <160> NUMBER OF SEQ ID NOS: 28

20 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
Corrected Diskette Needed

Cps, 1-2)

ERRORED SEQUENCES

3228 <210> SEQ ID NO: 28

3230 <211> LENGTH: 34

3231 <212> TYPE: DNA

3232 <213> ORGANISM: Artificial Sequence

3234 <220> FEATURE:

3235 <223> OTHER INFORMATION: Reverse primer to create T2609A mutation

3237 <400> SEQUENCE: 28

3239 gccctgggag gcctggctct ccacaaacat cgga

34

E--> 3242 1

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,561

DATE: 10/26/2004

TIME: 17:50:29

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10262004\J511561.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3242 M:254 E: No. of Bases conflict, this line has no nucleotides.

